

SEQUENCE LISTING

<110> Salkoff, Lawrence
Schreiber, Matthew
Silvia, Chris
The Washington University
ICAgene Inc.

<120> A pH Sensitive Potassium Channel in Spermatocytes

<130> 018512-000120US

<140> 09/176,664

<141> 1998-10-21

<150> US 60/063,138

<151> 1997-10-22

<150> US 60/076,172

<151> 1998-02-27

<160> 53

<170> PatentIn Ver. 2.0

<210> 1

<211> 1112

<212> PRT

<213> Mus musculus

<220>

<223> mouse Slo3 (mSlo3)

<220>

<221> VARIANT

<222> (5)

<223> polymorphic variant #2 Leu -> Ile

<220>

<221> VARIANT

<222> (21)

<223> polymorphic variant #1 Ile -> Val

<220>

<221> VARIANT

<222> (25)

<223> polymorphic variant #3 Ala -> Ser

<400> 1

Met Ser Gln Thr Leu Leu Asp Ser Leu Asn Gln Lys Glu Leu Thr Glu
1 5 10 15

Thr Ser Cys Thr Ile Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Leu
20 25 30

Ala Thr Phe Phe Gly Gly Leu Ile Ile Leu Phe Leu Phe Arg Ile Ala
35 40 45

Leu Lys Ser Ser Arg Ser Trp Lys Tyr Val Lys Gly Pro Arg Gly Leu
50 55 60

Leu	Glu	Leu	Phe	Ser	Ser	Arg	Arg	Ile	Glu	Ala	Asn	Pro	Leu	Arg	Lys
65					70					75					80
Leu	Tyr	Phe	His	Gly	Val	Phe	Arg	Gln	Arg	Ile	Glu	Met	Leu	Leu	Ser
				85					90					95	
Ala	Gln	Thr	Val	Val	Gly	Gln	Val	Leu	Val	Ile	Leu	Val	Phe	Val	Leu
			100					105					110		
Ser	Ile	Gly	Ser	Leu	Val	Ile	Tyr	Phe	Ile	Asn	Ser	Met	Asp	Pro	Val
		115					120					125			
Arg	Arg	Cys	Ser	Ser	Tyr	Glu	Asp	Lys	Ile	Val	His	Gly	Asp	Leu	Ser
	130					135					140				
Phe	Asn	Ala	Phe	Phe	Ser	Phe	Tyr	Phe	Gly	Leu	Arg	Phe	Trp	Ala	Ala
145					150					155					160
Glu	Asp	Lys	Ile	Lys	Phe	Trp	Leu	Glu	Met	Asn	Ser	Ile	Val	Asp	Ile
				165					170					175	
Phe	Thr	Ile	Pro	Pro	Thr	Phe	Ile	Ser	Tyr	Tyr	Leu	Lys	Ser	Asn	Trp
			180					185					190		
Leu	Gly	Leu	Arg	Phe	Leu	Arg	Ala	Leu	Arg	Leu	Leu	Glu	Leu	Pro	Lys
		195					200					205			
Ile	Leu	Gln	Ile	Leu	Gln	Val	Ile	Lys	Thr	Ser	Asn	Ser	Val	Lys	Leu
	210					215					220				
Ser	Lys	Leu	Leu	Ser	Ile	Val	Ile	Ser	Thr	Trp	Phe	Thr	Ala	Ala	Gly
225					230					235					240
Phe	Leu	His	Leu	Val	Glu	Asn	Ser	Gly	Asp	Pro	Trp	Leu	Asn	Gly	Arg
				245					250					255	
Asn	Ser	Gln	Thr	Met	Ser	Tyr	Phe	Glu	Ser	Ile	Tyr	Leu	Val	Thr	Ala
			260					265					270		
Thr	Met	Ser	Thr	Val	Gly	Phe	Gly	Asp	Val	Val	Ala	Lys	Thr	Ser	Leu
		275					280					285			
Gly	Arg	Ile	Phe	Ile	Val	Phe	Phe	Thr	Leu	Gly	Ser	Leu	Ile	Leu	Phe
	290					295					300				
Ala	Asn	Tyr	Ile	Pro	Glu	Met	Val	Glu	Leu	Phe	Ser	Thr	Arg	Lys	Lys
305					310					315					320
Tyr	Thr	Lys	Pro	Tyr	Glu	Ala	Val	Lys	Gly	Lys	Lys	Phe	Ile	Val	Val
				325					330					335	
Cys	Gly	Asn	Ile	Thr	Val	Asp	Ser	Val	Thr	Ala	Phe	Leu	Arg	Asn	Phe
			340					345					350		
Leu	His	Trp	Lys	Ser	Gly	Glu	Ile	Asn	Ile	Glu	Ile	Val	Phe	Leu	Gly
		355					360					365			
Glu	Thr	Leu	Pro	Cys	Leu	Glu	Leu	Glu	Thr	Leu	Leu	Lys	Cys	His	Thr
						375					380				

Ser	Cys	Thr	Asn	Phe	Val	Cys	Gly	Thr	Ala	Leu	Lys	Phe	Glu	Asp	Leu
385					390					395					400
Lys	Arg	Val	Ala	Val	Glu	Asn	Ser	Glu	Ala	Cys	Leu	Ile	Leu	Ala	Asn
				405					410					415	
His	Phe	Cys	Ser	Asp	Leu	His	Asp	Glu	Asp	Asn	Ser	Asn	Ile	Met	Arg
			420					425					430		
Val	Leu	Ser	Ile	Lys	Asn	Tyr	Tyr	Pro	Gln	Thr	Arg	Val	Ile	Ile	Gln
		435					440					445			
Ile	Leu	Gln	Ser	Gln	Asn	Lys	Val	Phe	Leu	Ser	Lys	Ile	Pro	Asn	Trp
	450					455					460				
Asp	Trp	Ser	Ala	Gly	Asp	Asn	Ile	Leu	Cys	Phe	Ala	Glu	Leu	Lys	Leu
465					470					475					480
Gly	Phe	Ile	Ala	Gln	Gly	Cys	Leu	Val	Pro	Gly	Leu	Cys	Thr	Phe	Leu
				485					490					495	
Thr	Thr	Leu	Phe	Ile	Glu	Gln	Asn	Gln	Lys	Val	Phe	Pro	Lys	His	Pro
			500					505					510		
Trp	Gln	Lys	His	Phe	Leu	Asn	Gly	Leu	Lys	Asn	Lys	Ile	Leu	Thr	Gln
		515					520					525			
Arg	Leu	Ser	Asn	Asp	Phe	Val	Gly	Met	Thr	Phe	Pro	Gln	Val	Ser	Arg
	530					535					540				
Leu	Cys	Phe	Val	Lys	Leu	Asn	Leu	Met	Leu	Ile	Ala	Ile	Gln	His	Lys
545					550					555					560
Pro	Phe	Phe	His	Ser	Cys	Cys	Thr	Leu	Ile	Leu	Asn	Pro	Ser	Ser	Gln
				565					570					575	
Val	Arg	Leu	Asn	Lys	Asp	Thr	Leu	Gly	Phe	Phe	Ile	Ala	Asp	Ser	Ser
			580					585					590		
Lys	Ala	Val	Lys	Arg	Ala	Phe	Phe	Tyr	Cys	Ser	Asn	Cys	His	Ser	Asp
		595					600					605			
Val	Cys	Asn	Pro	Glu	Leu	Ile	Gly	Lys	Cys	Asn	Cys	Lys	Ile	Lys	Ser
	610					615					620				
Arg	Gln	Gln	Leu	Ile	Ala	Pro	Thr	Ile	Met	Val	Met	Lys	Ser	Ser	Leu
625					630					635					640
Thr	Asp	Phe	Thr	Thr	Ser	Ser	His	Ile	His	Ala	Ser	Met	Ser	Thr	Glu
				645					650					655	
Ile	His	Thr	Cys	Phe	Ser	Arg	Glu	Gln	Pro	Ser	Leu	Ile	Thr	Ile	Thr
			660					665					670		
Thr	Asn	Arg	Pro	Thr	Thr	Asn	Asp	Thr	Val	Asp	Asp	Thr	Asp	Met	Leu
		675					680					685			
Asp	Ser	Ser	Gly	Met	Phe	His	Trp	Cys	Arg	Ala	Met	Pro	Leu	Asp	Lys
	690					695					700				

09019076 000000

Val Val Leu Lys Arg Ser Glu Lys Ala Lys His Glu Phe Gln Asn His
705 710 715 720

Ile Val Val Cys Val Phe Gly Asp Ala Gln Cys Thr Leu Val Gly Leu
725 730 735

Arg Asn Phe Val Met Pro Leu Arg Ala Ser Asn Tyr Thr Arg Gln Glu
740 745 750

Leu Lys Asp Ile Val Phe Ile Gly Ser Leu Glu Tyr Phe Gln Arg Glu
755 760 765

Trp Arg Phe Leu Arg Asn Phe Pro Lys Ile His Ile Met Pro Gly Ser
770 775 780

Ala Leu Tyr Met Gly Asp Leu Ile Ala Val Asn Val Glu Gln Cys Ser
785 790 795 800

Met Cys Val Ile Leu Ala Thr Pro Tyr Lys Ala Leu Ser Ser Gln Ile
805 810 815

Leu Val Asp Thr Glu Ala Ile Met Ala Thr Leu Asn Ile Gln Ser Leu
820 825 830

Arg Ile Thr Ser Pro Thr Pro Gly Ser Ser Lys Ser Glu Val Lys Pro
835 840 845

Ser Ser Ala Phe Asp Ser Lys Glu Arg Lys Gln Arg Tyr Lys Gln Ile
850 855 860

Pro Ile Leu Thr Glu Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu
865 870 875 880

Gln Met Gly Gly Leu Asp Gly Met Leu Lys Gly Thr Ser Leu His Leu
885 890 895

Ser Thr Ser Phe Ser Thr Gly Ala Val Phe Ser Asp Thr Phe Leu Asp
900 905 910

Ser Leu Leu Ala Thr Ser Phe Tyr Asn Tyr His Val Val Glu Leu Leu
915 920 925

Gln Met Leu Val Thr Gly Gly Ile Ser Ser Glu Met Glu His Tyr Leu
930 935 940

Val Lys Glu Lys Pro Tyr Lys Thr Thr Asp Asp Tyr Glu Ala Ile Lys
945 950 955 960

Ser Gly Arg Thr Arg Cys Lys Leu Gly Leu Leu Ser Leu Asp Gln Thr
965 970 975

Val Leu Ser Gly Ile Asn Pro Arg Lys Thr Phe Gly Gln Leu Phe Cys
980 985 990

Gly Ser Leu Asp Asn Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Met
995 1000 1005

Ile Asp Glu Glu Glu Pro Ser Gln Glu His Lys Arg Phe Val Ile Thr
1010 1015 1020

Arg Pro Ser Asn Glu Cys His Leu Leu Pro Ser Asp Leu Val Phe Cys
 1025 1030 1035 1040

Ala Ile Pro Phe Asn Thr Thr Cys Gly Lys Ser Asp Ser Ser Pro Phe
 1045 1050 1055

Asn Phe Arg Leu Lys Thr Thr Leu Gln Thr Arg Arg Arg His Trp Pro
 1060 1065 1070

Arg Gly Arg Ile Ser Ser Ile Arg Thr Met Pro Thr Ser Pro Thr Ile
 1075 1080 1085

Phe Thr Gln Ser Thr Thr Arg Glu Arg Gly Gly Leu Ser Thr Thr Thr
 1090 1095 1100

Pro Glu Ser Ile Leu Trp Thr Arg
 1105 1110

<210> 2
 <211> 3339
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse Slo3 (mSlo3)

<400> 2
 atgtctcaaa cattgctaga cagtttaaatt cagaaggagt tgacggaaac gtcattgtaca 60
 atcgaaatcc aggcagcggt cattctttcc tccttggcga ctttcttcgg gggactcatc 120
 atcttattcc ttttcagaat agccttgaaa agctcaagaa gttggaaata cgtcaagggg 180
 ccaagaggac tcttggaact attctcatca cgtagaatcg aggctaattc tttgaggaaa 240
 ctttactttc atggagtatt tcgtcagcgc atcgaaatgc tgctttctgc acagaccgtc 300
 gtggggcaag tgttggtgat ccttgtcttt gtactaagca tcgggtctct tgtgatctat 360
 ttcatcaatt caatggatcc tgttcgaagg tgttcttcat atgaagacaa aattgtccat 420
 ggggatttga gtttcaacgc tttcttttagc ttctattttg ggttgagggt ttgggcagct 480
 gaagacaaga tcaagttctg gttggagatg aattcaattg tagacatttt taccatcccg 540
 ccaaccttta tttcttatta tttgaagagt aattggctag gtttgagatt tctaagagct 600
 ctgcggttgc tcgaactccc taaaatctta cagatcctac aagtcaccaa gaccagcaat 660
 tcagtgaagc ttcccaaact gttgtcaata gttatcagta cctgggttcac ggcagcagga 720
 ttccttcacc tgggtggaaaa ttctggtgac ccctgggtca acggaagaaa ctacagact 780
 atgtcatact ttgagtctat ttatctggtg acagcaacaa tgtcaactgt tggctttggg 840
 gacgtggttg ccaagacatc cctaggacgg attttcattg ttttcttcac ccttgggagt 900
 ttgatactat ttgcaaacta cattccagaa atgggtggagc tcttttctac caggaagaaa 960
 tacaccaagc cctacgaagc agtcaaagga aaaaagttca tcgtggtctg tggaaacatc 1020
 acagttgaca gtgttactgc tttcctgagg aattttctcc actggaagtc cggggaaatc 1080
 aatattgaga tcgtattcct tggagagact ctcccttgct tggaaactgga gaccttactg 1140
 aagtgccaca catcctgtac caacttcgta tgccgcaccg cactgaagtt cgaggatctg 1200
 aagcgagttg cagtggagaa ctcggaggcg tgccctgattc tagccaacca tttctgtagt 1260
 gacttacatg acgaagacaa ctcaaacatt atgagggtgc tctcgatcaa gaactattat 1320
 ccacagacca gagtcatcat tcagatactt cagtctcaaa acaaggtttt cctgtcaaaa 1380
 atccccaact gggactggag tgctggagac aatatcctct gctttgcaga gctaaagctc 1440
 ggatttatcg cccaaggctg cttggtgcca gggctgtgca cctttctcac gactctgttc 1500
 attgaacaaa accaaaaggt ttttcctaaa catccctggc aaaaacattt cttgaatggc 1560
 ttgaagaaca agattctgac acagcgctc tctaacgact tcgtggggat gacatttccc 1620
 caggtctccc ggctctgctt tgtgaagcta aatctcatgc tgatcgccat ccaacacaag 1680
 cccttctttc acagttgttg cactctgata ctaaaccat catcccaagt gaggctgaat 1740
 aaggacacct tagggttctt cattgctgac tctccaaaag ccgtcaaaag ggctttcttt 1800
 tactgttcca actgtcacag cgatgtgtgc aatcctgagc taattggaaa gtgtaactgt 1860
 aaaatcaaga gccgacaaca actcatagca ccgaccatca tgggtgatgaa aagcagcttg 1920
 accgatttca ccacttcttc acacatccac gcttctatgt caacagaaat tcacacttgt 1980

0515076.030000

THE UNIVERSITY OF CHICAGO

<223> Description of Artificial Sequence:mSlo3 primer

<400> 9

ttccgttgag ccaggggtca ccagaatt

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 10

tctgctttgt gaagctaaat ct

<210> 11

$\langle 211 \rangle$ 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 11

tttcaaagcc tcttttagcgg taa

<210> 12

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 12

ttatgcctgg atctgcactc tacatg

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 primer

<400> 13

atagtttccg tctactaccg aaa

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

Chronic Disease

<223> Description of Artificial Sequence:hSlo3 primer

24

ggcagcgctc attctttcct cctt

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence:hSlo3 primer

24

tqcccaaaac ctcaacccaa aata

<210> 16

<211> 1105

<212> PRT

<213> Homo sapiens

<220>

<223> human Slo3-1 (hSlo3-1)

$\langle 220 \rangle$

<221> VARIANT

<222> (6)

<223> polymorphic variant #2 Leu -> Ile

$\langle 220 \rangle$

<221> VARIANT

<222> (23)

<223> polymorphic variant #1 Ile -> Val

$\langle 220 \rangle$

<221> VARIANT

<222> (25)

<223> polymorphic variant #3 Ala -> Ser

<400> 16

Met Phe Gln Thr Lys Leu Arg Asn Glu Thr Trp Glu Asp Leu Pro Lys
1 5 10 15

Met Ser Cys Thr Thr Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Phe
20 25 30

Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Leu Ile Phe Arg Leu Ile
35 40 45

Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
50 55 60

Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
65 70 75 80

Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
85 90 95

Pro Leu Arg Ala Ser Asn Tyr Thr Arg Lys Glu Leu Lys Asp Ile Val
 740 745 750
 Phe Ile Gly Ser Leu Asp Tyr Leu Gln Arg Glu Trp Arg Phe Leu Arg
 755 760 765
 Asn Phe Pro Gln Ile Tyr Ile Leu Pro Gly Cys Ala Leu Tyr Ser Gly
 770 775 780
 Asp Leu His Ala Ala Asn Ile Glu Gln Cys Ser Met Cys Ala Val Leu
 785 790 795 800
 Ser Pro Pro Pro Gln Pro Ser Ser Asn Gln Thr Leu Val Asp Thr Glu
 805 810 815
 Ala Ile Met Ala Thr Leu Thr Ile Gly Ser Leu Gln Ile Asp Ser Ser
 820 825 830
 Ser Asp Pro Ser Pro Ser Val Ser Glu Glu Thr Pro Gly Tyr Thr Asn
 835 840 845
 Gly His Asn Glu Lys Ser Asn Cys Arg Lys Val Pro Ile Leu Thr Glu
 850 855 860
 Leu Lys Asn Pro Ser Asn Ile His Phe Ile Glu Gln Leu Gly Gly Leu
 865 870 875 880
 Glu Gly Ser Leu Gln Glu Thr Asn Leu His Leu Ser Thr Ala Phe Ser
 885 890 895
 Thr Gly Thr Val Phe Ser Ser Ser Phe Leu Asp Ser Leu Leu Ala Thr
 900 905 910
 Ala Phe Tyr Asn Tyr His Val Leu Glu Leu Leu Gln Met Leu Val Thr
 915 920 925
 Gly Gly Val Ser Ser Gln Leu Glu Gln His Leu Asp Lys Asp Lys Val
 930 935 940
 Tyr Gly Val Ala Asp Ser Cys Thr Ser Leu Leu Ser Gly Arg Asn Arg
 945 950 955 960
 Cys Lys Leu Gly Leu Leu Ser Leu His Glu Thr Ile Leu Ser Asp Val
 965 970 975
 Asn Pro Arg Asn Thr Phe Gly Gln Leu Phe Cys Gly Ser Leu Asp Leu
 980 985 990
 Phe Gly Ile Leu Cys Val Gly Leu Tyr Arg Ile Ile Asp Glu Glu Glu
 995 1000 1005
 Leu Asn Pro Glu Asn Lys Arg Phe Val Ile Thr Arg Pro Ala Asn Glu
 1010 1015 1020
 Phe Lys Leu Leu Pro Ser Asp Leu Val Phe Cys Ala Ile Pro Phe Ser
 1025 1030 1035 1040
 Thr Ala Cys Tyr Lys Arg Asn Glu Glu Phe Ser Leu Gln Lys Ser Tyr
 1045 1050 1055

Glu Ile Val Asn Lys Ala Ser Gln Thr Thr Glu Asp Thr Phe Arg His
 1060 1065 1070

Lys Leu Ser Ser His Pro Leu Ile Gln Leu Leu Arg His Cys Ile His
 1075 1080 1085

Gln Ser Ile Leu Thr Ser Arg Glu Leu Thr Pro Ser Leu Phe Leu Ser
 1090 1095 1100

Lys
 1105

<210> 17
 <211> 3319
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human Slo3-1 (hSlo3-1)

<400> 17
 atgtttcaga ctaagctacg aaatgaaact tgggaagact tgccaaaaat gtccctgcaca 60
 actgagatcc aagcagcatt cattctctct tcctttgtga ccttcttcag tggactcatc 120
 atcctgttga tcttcaggct gatctggaga tctgttaaaa aatggcaaat catcaaggga 180
 acaggaatta tcttggaact gttcacatca ggtaccatcg ctaggagcca tgtaagaagc 240
 ctccacttcc agggacaatt tctgtatcat atagaaatgt tgctttcagc ccagaccttt 300
 gtggggcaag tgttggtgat ccttgtcttt gtaactaagca ttgggtctct tataatctat 360
 ttcattcaatt ctgctgaccc tgttggaagc tgttcatcat atgaagacaa aaccatttct 420
 attgatttgg ttttcaatgc tttctttagt ttctattttg gattgaggtt tatggcagct 480
 gatgacaaga tcaagttctg gctggagatg aattcaatcg tagacatctt taccatccca 540
 ccaaccttta tttcttatta tttgaagagc aattggctag gtttaagggt cctaagagcc 600
 ttgctgcctgc tagaactccc tcaaactctg caaattctac gagccatcaa gaccagtaac 660
 tcagtgaagt tttccaaact gctgtcaata attctcagta cctgggtcac agctgctgga 720
 ttcattcacc tgggtgaaaa ttctggtgat ccctggctca aaggtagaaa ttcacagaat 780
 atatcatatt ttgagtcaat ttacctggtc atggcaacaa cgtcaaccgt tggatttgga 840
 gatgtggtag ccaagacatc cttaggacgg accttcatca tgttcttcac actggggagt 900
 ttgatattat ttgcgaacta tatacctgaa atggtggaac tgtttgctaa caagaggaaa 960
 tacaccagtt cmtatgaagc actcaaagga aagaagttta ttgtggtctg tggaaacatc 1020
 actgtggaca gtgtgaccgc tttcctgagg aatttctctc gcgacaagtc aggagagatc 1080
 aacactgaaa ttgttttctc gggagaaaacc cctccttctt tggaacttga aaccatattt 1140
 aaatgctact tggcctacac aacgttcatt tctggatctg caatgaagtg ggaggatctg 1200
 aggcgagttg cgggtggaatc tgcagaggca tgcctgatta tagccaatcc tttgtgcagt 1260
 gattcccatg ctgaagatat ttccaacatt atgaggggtgc tctctatcaa gaactatgat 1320
 tctaccacca gaatcatcat acagatactg caatcccata acaaggttta tctgccaaag 1380
 attcccagct ggaactggga caccggagac aacatcatct gctttgctga attaaaactt 1440
 ggatttatcg cccaaggctg tttggtgcca ggcttgtgta ccttcctaac atctctattt 1500
 gtggagcaaaa acaaaaaggt tatgcctaaa cagacctgga agaaacactt cttgaatagc 1560
 atgaaaaaca aaattctgac ccaacgtctc tctgatgact ttgctggaat gagctttcct 1620
 gaagttgccc ggctctgctt tctgaagatg tacctctgtt tgatagccat cgaatacaag 1680
 tccctcttta cggatgggtt ctgtggtctg atactaaatc cacctccaca agtgaggata 1740
 cgtaagaaca cattagggtt ctttatttgc gaaactccaa aggacgtcag aagagccttg 1800
 ttttactgtt cagtctgtca tgatgatgtg ttcattcctg agctaattac aaactgtggc 1860
 tgcaaaaagca gaagccggca gcacatcaca gtgccatcgg taaagagaat gaaaaaatgt 1920
 ctgaaggga tctcctctcg tatatcaggg caggattctc cgccaagggt atctgcaagc 1980
 acttcgagca tatcaaactt caccaccagg actcttcaac atgatgtaga acaagattct 2040
 gaccagcttg atagcagtg gatgtttcac tgggtgcaaac accatattgt agcatgtgta 2100
 actctgaaac gaactggcaa gtcaaagtat aagtttcgga accatattgt agcatgtgta 2160
 tttggagatg cccactcagc cccgatgggg cttcggaact ttgtaatgcc cttgagagcc 2220
 agcaactata ccaggaagga gctgaaggac atagtgttca ttgggtctct ggactatcta 2280
 cagagagaat ggcgatttct ccggaatttt cccagatat acattctgcc tggatgtgca 2340

```

ctttattctg gagacctcca tgcggccaac atagagcaat gctccatgtg tgctgtcttg 2400
tccccccac cccagccatc aagcaaccag actttggtag acacagaagc catcatggca 2460
accctcacca tcggatcctt gcaaattgac tcctcctctg acccgtcacc ctcaagtgtca 2520
gaggagactc cagggttacac aaatggacat aatgagaaat caaactgccg aaaagtccct 2580
atccttactg aactgaaaaa tccttccaac attcacttta ttgaacagct tgggtggactg 2640
gaagggtccc tccaagaaac aaatctgcat ctccagcactg ccttttctac gggcactggt 2700
ttttccagca gcttcttgga ttctctgctg gccacggcct tctacaatta tcatgtcctg 2760
gaattgcttc agatgctggt gacaggagga gtaagtctc agctggaaca acatttagat 2820
aaggataaag tctatggtgt ggcagatagc tgcacgtcgc tcttgctggt aagaaaccgg 2880
tgtaagctgg ggcttctgtc cttacacgaa accattttat cagacgttaa tccaagaaac 2940
acctttggac aactgttctg tggctcatta gatctttttg gaatcctgtg tgttggctta 3000
taccgaataa ttgatgaaga ggagctcaac ccagaaaaca aaaggtttgt gatcaccggg 3060
ccagccaatg agttcaagct gctgccttca gatcttgtgt tttgtgccat acccttcagc 3120
actgcttggt ataaaaggaa tgaagagttc tcattgcaaa agtcatatga aattgtaaat 3180
aaagcatcac agacaacaga ggacacattc agacacaaat tgctcctcca cccattgatt 3240
cagttactga gacattgtat tcaccagtct attcttacca gccgagaact aactccctct 3300
cttttcttaa gcaaatagg 3319

```

<210> 18

<211> 1081

<212> PRT

<213> Homo sapiens

<220>

<223> human hSlo3-2 (hSlo3-2)

<400> 18

```

Met Phe Gln Thr Lys Leu Arg Asn Glu Thr Trp Glu Asp Leu Pro Lys
 1             5             10             15

Met Ser Cys Thr Thr Glu Ile Gln Ala Ala Phe Ile Leu Ser Ser Phe
          20          25          30

Val Thr Phe Phe Ser Gly Leu Ile Ile Leu Leu Ile Phe Arg Leu Ile
      35          40          45

Trp Arg Ser Val Lys Lys Trp Gln Ile Ile Lys Gly Thr Gly Ile Ile
 50          55          60

Leu Glu Leu Phe Thr Ser Gly Thr Ile Ala Arg Ser His Val Arg Ser
65          70          75          80

Leu His Phe Gln Gly Gln Phe Arg Asp His Ile Glu Met Leu Leu Ser
          85          90          95

Ala Gln Thr Phe Val Gly Gln Val Leu Val Ile Leu Val Phe Val Leu
      100          105          110

Ser Ile Gly Ser Leu Ile Ile Tyr Phe Ile Asn Ser Ala Asp Pro Val
      115          120          125

Gly Ser Cys Ser Ser Tyr Glu Asp Lys Thr Ile Pro Ile Asp Leu Val
      130          135          140

Phe Asn Ala Phe Phe Ser Phe Tyr Phe Gly Leu Arg Phe Met Ala Ala
      145          150          155          160

Asp Asp Lys Ile Lys Phe Trp Leu Glu Met Asn Ser Ile Val Asp Ile
      165          170          175

```


CONFIDENTIAL

1.

```
<210> 20
<211> 1134
<212> PRT
<213> Mus musculus
```

```
<220>
<223> mouse Slo3 (mSlo3)
```

Thr	Met	Ser	Thr	Val	Gly	Phe	Gly	Asp	Val	Val	Ala	Lys	Thr	Ser	Leu
		275					280					285			
Gly	Arg	Ile	Phe	Ile	Val	Phe	Phe	Thr	Leu	Gly	Ser	Leu	Ile	Leu	Phe
	290					295					300				
Ala	Asn	Tyr	Ile	Pro	Glu	Met	Val	Glu	Leu	Phe	Ser	Thr	Arg	Lys	Lys
305					310					315					320
Tyr	Thr	Lys	Pro	Tyr	Glu	Ala	Val	Lys	Gly	Lys	Lys	Phe	Ile	Val	Val
				325					330					335	
Cys	Gly	Asn	Ile	Thr	Val	Asp	Ser	Val	Thr	Ala	Phe	Leu	Arg	Asn	Phe
			340					345					350		
Leu	His	Trp	Lys	Ser	Gly	Glu	Ile	Asn	Ile	Glu	Ile	Val	Phe	Leu	Gly
		355					360					365			
Glu	Thr	Leu	Pro	Cys	Leu	Glu	Leu	Glu	Thr	Leu	Leu	Lys	Cys	His	Thr
	370					375					380				
Ser	Cys	Thr	Asn	Phe	Val	Cys	Gly	Thr	Ala	Leu	Lys	Phe	Glu	Asp	Leu
385					390					395					400
Lys	Arg	Val	Ala	Val	Glu	Asn	Ser	Glu	Ala	Cys	Leu	Ile	Leu	Ala	Asn
				405					410					415	
His	Phe	Cys	Ser	Asp	Leu	His	Asp	Glu	Asp	Asn	Ser	Asn	Ile	Met	Arg
			420					425					430		
Val	Leu	Ser	Ile	Lys	Asn	Tyr	Tyr	Pro	Gln	Thr	Arg	Val	Ile	Ile	Gln
		435					440					445			
Ile	Leu	Gln	Ser	Gln	Asn	Lys	Val	Phe	Leu	Ser	Lys	Ile	Pro	Asn	Trp
	450					455					460				
Asp	Trp	Ser	Ala	Gly	Asp	Asn	Ile	Leu	Cys	Phe	Ala	Glu	Leu	Lys	Leu
465					470					475					480
Gly	Phe	Ile	Ala	Gln	Gly	Cys	Leu	Val	Pro	Gly	Leu	Cys	Thr	Phe	Leu
				485					490					495	
Thr	Thr	Leu	Phe	Ile	Glu	Gln	Asn	Gln	Lys	Val	Phe	Pro	Lys	His	Pro
			500					505					510		
Trp	Gln	Lys	His	Phe	Leu	Asn	Gly	Leu	Lys	Asn	Lys	Ile	Leu	Thr	Gln
		515					520					525			
Arg	Leu	Ser	Asn	Asp	Phe	Val	Gly	Met	Thr	Phe	Pro	Gln	Val	Ser	Arg
	530					535					540				
Leu	Cys	Phe	Val	Lys	Leu	Asn	Leu	Met	Leu	Ile	Ala	Ile	Gln	His	Lys
545					550					555					560
Pro	Phe	Phe	His	Ser	Cys	Cys	Thr	Leu	Ile	Leu	Asn	Pro	Ser	Ser	Gln
				565					570					575	
Val	Arg	Leu	Asn	Lys	Asp	Thr	Leu	Gly	Phe	Phe	Ile	Ala	Asp	Ser	Ser
			580					585					590		

Lys	Ala	Val	Lys	Arg	Ala	Phe	Phe	Tyr	Cys	Ser	Asn	Cys	His	Ser	Asp
		595					600								605
Val	Cys	Asn	Pro	Glu	Leu	Ile	Gly	Lys	Cys	Asn	Cys	Lys	Ile	Lys	Ser
	610					615					620				
Arg	Gln	Gln	Leu	Ile	Ala	Pro	Thr	Ile	Met	Val	Met	Lys	Ser	Ser	Leu
625					630					635					640
Thr	Asp	Phe	Thr	Thr	Ser	Ser	His	Ile	His	Ala	Ser	Met	Ser	Thr	Glu
				645					650					655	
Ile	His	Thr	Cys	Phe	Ser	Arg	Glu	Gln	Pro	Ser	Leu	Ile	Thr	Ile	Thr
			660					665					670		
Thr	Asn	Arg	Pro	Thr	Thr	Asn	Asp	Thr	Val	Asp	Asp	Thr	Asp	Met	Leu
		675					680					685			
Asp	Ser	Ser	Gly	Met	Phe	His	Trp	Cys	Arg	Ala	Met	Pro	Leu	Asp	Lys
	690					695					700				
Val	Val	Leu	Lys	Arg	Ser	Glu	Lys	Ala	Lys	His	Glu	Phe	Gln	Asn	His
705					710					715					720
Ile	Val	Val	Cys	Val	Phe	Gly	Asp	Ala	Gln	Cys	Thr	Leu	Val	Gly	Leu
				725					730					735	
Arg	Asn	Phe	Val	Met	Pro	Leu	Arg	Ala	Ser	Asn	Tyr	Thr	Arg	Gln	Glu
			740					745					750		
Leu	Lys	Asp	Ile	Val	Phe	Ile	Gly	Ser	Leu	Glu	Tyr	Phe	Gln	Arg	Glu
		755					760					765			
Trp	Arg	Phe	Leu	Arg	Asn	Phe	Pro	Lys	Ile	His	Ile	Met	Pro	Gly	Ser
	770					775					780				
Ala	Leu	Tyr	Met	Gly	Asp	Leu	Ile	Ala	Val	Asn	Val	Glu	Gln	Cys	Ser
785					790					795					800
Met	Cys	Val	Ile	Leu	Ala	Thr	Pro	Tyr	Lys	Ala	Leu	Ser	Ser	Gln	Ile
			805						810					815	
Leu	Val	Asp	Thr	Glu	Ala	Ile	Met	Ala	Thr	Leu	Asn	Ile	Gln	Ser	Leu
			820					825					830		
Arg	Ile	Thr	Ser	Pro	Thr	Pro	Gly	Ser	Ser	Lys	Ser	Glu	Val	Lys	Pro
		835					840					845			
Ser	Ser	Ala	Phe	Asp	Ser	Lys	Glu	Arg	Lys	Gln	Arg	Tyr	Lys	Gln	Ile
	850					855					860				
Pro	Ile	Leu	Thr	Glu	Leu	Lys	Asn	Pro	Ser	Asn	Ile	His	Phe	Ile	Glu
865					870					875					880
Gln	Met	Gly	Gly	Leu	Asp	Gly	Met	Leu	Lys	Gly	Thr	Ser	Leu	His	Leu
				885					890					895	
Ser	Thr	Ser	Phe	Ser	Thr	Gly	Ala	Val	Phe	Ser	Asp	Thr	Phe	Leu	Asp
			900					905					910		

Asp	Asp	Val	Asn	Val	Glu	Ile	Val	Phe	Leu	His	Asn	Ile	Ser	Pro	Asn
370						375					380				
Leu	Glu	Leu	Glu	Ala	Leu	Phe	Lys	Arg	His	Phe	Thr	Gln	Val	Glu	Phe
385					390					395					400
Tyr	Gln	Gly	Ser	Val	Leu	Asn	Pro	His	Asp	Leu	Ala	Arg	Val	Lys	Ile
				405					410					415	
Glu	Ser	Ala	Asp	Ala	Cys	Leu	Ile	Leu	Ala	Asn	Lys	Tyr	Cys	Ala	Asp
			420					425					430		
Pro	Asp	Ala	Glu	Asp	Ala	Ser	Asn	Ile	Met	Arg	Val	Ile	Ser	Ile	Lys
		435					440					445			
Asn	Tyr	His	Pro	Lys	Ile	Arg	Ile	Ile	Thr	Gln	Met	Leu	Gln	Tyr	His
	450					455					460				
Asn	Lys	Ala	His	Leu	Leu	Asn	Ile	Pro	Ser	Trp	Asn	Trp	Lys	Glu	Gly
465					470					475					480
Asp	Asp	Ala	Ile	Cys	Leu	Ala	Glu	Leu	Lys	Leu	Gly	Phe	Ile	Ala	Gln
				485					490					495	
Ser	Cys	Leu	Ala	Gln	Gly	Leu	Ser	Thr	Met	Leu	Ala	Asn	Leu	Phe	Ser
			500					505					510		
Met	Arg	Ser	Phe	Ile	Lys	Ile	Glu	Glu	Asp	Thr	Trp	Gln	Lys	Tyr	Tyr
		515					520					525			
Leu	Glu	Gly	Val	Ser	Asn	Glu	Met	Tyr	Thr	Glu	Tyr	Leu	Ser	Ser	Ala
	530					535					540				
Phe	Val	Gly	Leu	Ser	Phe	Pro	Thr	Val	Cys	Glu	Leu	Cys	Phe	Val	Lys
545					550					555					560
Leu	Lys	Leu	Leu	Met	Ile	Ala	Ile	Glu	Tyr	Lys	Ser	Ala	Asn	Arg	Glu
				565					570					575	
Ser	Arg	Ile	Leu	Ile	Asn	Pro	Gly	Asn	His	Leu	Lys	Ile	Gln	Glu	Gly
			580					585					590		
Thr	Leu	Gly	Phe	Phe	Ile	Ala	Ser	Asp	Ala	Lys	Glu	Val	Lys	Arg	Ala
		595					600					605			
Phe	Phe	Tyr	Cys	Lys	Ala	Cys	His	Asp	Asp	Val	Thr	Asp	Pro	Lys	Arg
	610					615					620				
Ile	Lys	Lys	Cys	Gly	Cys	Arg	Arg	Leu	Ile	Tyr	Phe	Glu	Asp	Glu	Gln
625					630					635					640
Pro	Pro	Thr	Leu	Ser	Pro	Lys	Lys	Lys	Gln	Arg	Asn	Gly	Gly	Met	Arg
				645					650					655	
Asn	Ser	Pro	Asn	Thr	Ser	Pro	Lys	Leu	Met	Arg	His	Asp	Pro	Leu	Leu
			660					665					670		
Ile	Pro	Gly	Asn	Asp	Gln	Ile	Asp	Asn	Met	Asp	Ser	Asn	Val	Lys	Lys
		675					680					685			

Thr Tyr Asn Met Leu Cys Phe Gly Ile Tyr Arg Leu Arg Asp Ala His
1010 1015 1020

Leu Ser Thr Pro Ser Gln Cys Thr Lys Arg Tyr Val Ile Thr Asn Pro
1025 1030 1035 1040

Pro Tyr Glu Phe Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met
1045 1050 1055

Gln Phe Asp His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser
1060 1065 1070

Ser His Ser Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser
1075 1080 1085

Ile Pro Ser Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser
1090 1095 1100

Arg Asp Lys Gln Asn Ala Thr Arg Met Thr Arg Met Gly Gln Ala Glu
1105 1110 1115 1120

Lys Lys Trp Phe Thr Asp Glu Pro Asp Asn Ala Tyr Pro Arg Asn Ile
1125 1130 1135

Gln Ile Lys Pro Met Ser Thr His Met Ala Asn Gln Ile Asn Gln Tyr
1140 1145 1150

Lys Ser Thr Ser Ser Leu Ile Pro Pro Ile Arg Glu Val Glu Asp Glu
1155 1160 1165

Cys Glu Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met Gln Phe Asp
1170 1175 1180

His Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser Ser His Ser
1185 1190 1195 1200

Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser Ile Pro Ser
1205 1210 1215

Thr Ala Asn Arg Pro Asn Arg Pro Lys Ser Arg Glu Ser Arg Asp Lys
1220 1225 1230

Gln Asn Ala Thr
1235

<210> 22

<211> 1262

<212> PRT

<213> Drosophila sp.

<220>

<223> Drosophila Slol (dSlol)

<400> 22

Met Ala Ser Gly Leu Ile Asp Thr Asn Phe Ser Ser Thr Leu Ala Asn
1 5 10 15

Gly Met Ser Gly Cys Asp Gln Ser Thr Val Glu Pro Leu Ala Asp Asp
20 25 30

Pro	Thr	Asp	Ser	Pro	Phe	Asp	Ala	Asp	Asp	Cys	Leu	Lys	Val	Arg	Lys
		35						40				45			
Tyr	Trp	Cys	Phe	Leu	Leu	Ser	Ser	Ile	Phe	Thr	Phe	Leu	Ala	Gly	Leu
	50					55					60				
Leu	Val	Val	Leu	Leu	Trp	Arg	Ala	Phe	Ala	Phe	Val	Ser	Cys	Arg	Lys
	65				70					75					80
Glu	Pro	Asp	Leu	Gly	Pro	Asn	Asp	Pro	Lys	Gln	Lys	Glu	Gln	Lys	Ala
				85					90					95	
Ser	Arg	Asn	Lys	Gln	Glu	Phe	Glu	Gly	Thr	Phe	Met	Thr	Glu	Ala	Lys
			100					105					110		
Asp	Trp	Ala	Gly	Glu	Leu	Ile	Ser	Gly	Gln	Thr	Thr	Thr	Gly	Arg	Ile
		115					120					125			
Leu	Val	Val	Leu	Val	Phe	Ile	Leu	Ser	Ile	Ala	Ser	Leu	Ile	Ile	Tyr
	130					135					140				
Phe	Val	Asp	Ala	Ser	Ser	Glu	Glu	Val	Glu	Arg	Cys	Gln	Lys	Trp	Ser
	145				150					155					160
Asn	Asn	Ile	Thr	Gln	Gln	Ile	Asp	Leu	Ala	Phe	Asn	Ile	Phe	Phe	Met
				165					170					175	
Val	Tyr	Phe	Phe	Ile	Arg	Phe	Ile	Ala	Ala	Ser	Asp	Lys	Leu	Trp	Phe
			180					185					190		
Met	Leu	Glu	Met	Tyr	Ser	Phe	Val	Asp	Tyr	Phe	Thr	Ile	Pro	Pro	Ser
		195					200					205			
Phe	Val	Ser	Ile	Tyr	Leu	Asp	Arg	Thr	Trp	Ile	Gly	Leu	Arg	Phe	Leu
	210					215					220				
Arg	Ala	Leu	Arg	Leu	Met	Thr	Val	Pro	Asp	Ile	Leu	Gln	Tyr	Leu	Asn
	225				230					235					240
Val	Leu	Lys	Thr	Ser	Ser	Ser	Ile	Arg	Leu	Ala	Gln	Leu	Val	Ser	Ile
				245					250					255	
Phe	Ile	Ser	Val	Trp	Leu	Thr	Ala	Ala	Gly	Ile	Ile	His	Leu	Leu	Glu
			260					265					270		
Asn	Ser	Gly	Asp	Pro	Leu	Asp	Phe	Asn	Asn	Ala	His	Arg	Leu	Ser	Tyr
		275					280					285			
Trp	Thr	Cys	Val	Tyr	Phe	Leu	Ile	Val	Thr	Met	Ser	Thr	Val	Gly	Tyr
	290					295					300				
Gly	Asp	Val	Tyr	Cys	Glu	Thr	Val	Leu	Gly	Arg	Thr	Phe	Leu	Val	Phe
	305				310					315					320
Phe	Leu	Leu	Val	Gly	Leu	Ala	Val	Phe	Ala	Ser	Trp	Ile	Pro	Glu	Ile
				325					330					335	
Thr	Glu	Leu	Ala	Ala	Gln	Arg	Ser	Lys	Tyr	Gly	Gly	Thr	Tyr	Ser	Lys
			340					345					350		

Leu	Asn	Arg	Asn	Val	Arg	Arg	Pro	Asn	Gly	Thr	Gly	Asn	Gly	Thr	Gly	
	675						680					685				
Gly	Met	His	His	Met	Asn	Ser	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
	690					695					700					
Ala	Ala	Gly	Lys	Gln	Val	Asn	Lys	Val	Lys	Pro	Thr	Val	Asn	Val	Ser	
705					710					715					720	
Arg	Gln	Val	Glu	Gly	Gln	Val	Ile	Ser	Pro	Ser	Gln	Tyr	Asn	Arg	Pro	
				725					730					735		
Thr	Ser	Arg	Ser	Ser	Gly	Thr	Gly	Thr	Gln	Asn	Gln	Asn	Gly	Gly	Val	
			740					745					750			
Ser	Leu	Pro	Ala	Gly	Ile	Ala	Asp	Asp	Gln	Ser	Lys	Asp	Phe	Asp	Phe	
		755					760					765				
Glu	Lys	Thr	Glu	Met	Lys	Tyr	Asp	Ser	Thr	Gly	Met	Phe	His	Trp	Ser	
	770					775					780					
Pro	Ala	Lys	Ser	Leu	Gln	Asp	Cys	Ile	Leu	Asp	Arg	Asn	Gln	Ala	Ala	
785					790					795					800	
Met	Thr	Val	Leu	Asn	Gly	His	Val	Val	Val	Cys	Leu	Phe	Ala	Asp	Pro	
				805					810					815		
Asp	Ser	Pro	Leu	Ile	Gly	Leu	Arg	Asn	Leu	Val	Met	Pro	Leu	Arg	Ala	
			820					825					830			
Ser	Asn	Phe	His	Tyr	His	Glu	Leu	Lys	His	Val	Val	Ile	Val	Gly	Ser	
		835					840					845				
Val	Asp	Tyr	Ile	Arg	Arg	Glu	Trp	Lys	Met	Leu	Gln	Asn	Leu	Pro	Lys	
	850					855					860					
Ile	Ser	Val	Leu	Asn	Gly	Ser	Pro	Leu	Ser	Arg	Ala	Asp	Leu	Arg	Ala	
865					870					875					880	
Val	Asn	Val	Asn	Leu	Cys	Asp	Met	Cys	Cys	Ile	Leu	Ser	Ala	Lys	Val	
				885				890						895		
Pro	Ser	Asn	Asp	Asp	Pro	Thr	Leu	Ala	Asp	Lys	Glu	Ala	Ile	Leu	Ala	
			900					905					910			
Ser	Leu	Asn	Ile	Lys	Ala	Met	Thr	Phe	Asp	Asp	Thr	Ile	Gly	Val	Leu	
		915					920					925				
Ser	Gln	Arg	Gly	Pro	Glu	Phe	Asp	Asn	Leu	Ser	Ala	Thr	Ala	Gly	Ser	
	930					935					940					
Pro	Ile	Val	Leu	Gln	Arg	Arg	Gly	Ser	Val	Tyr	Gly	Ala	Asn	Val	Pro	
945					950					955					960	
Met	Ile	Thr	Glu	Leu	Val	Asn	Asp	Gly	Asn	Val	Gln	Phe	Leu	Asp	Gln	
				965					970					975		
Asp	Asp	Asp	Asp	Asp	Pro	Asp	Thr	Glu	Leu	Tyr	Leu	Thr	Gln	Pro	Phe	
				980				985					990			

Ala Cys Gly Thr Ala Phe Ala Val Ser Val Leu Asp Ser Leu Met Ser
 995 1000 1005

Thr Thr Tyr Phe Asn Gln Asn Ala Leu Thr Leu Ile Arg Ser Leu Ile
 1010 1015 1020

Thr Gly Gly Ala Thr Pro Glu Leu Glu Leu Ile Leu Ala Glu Gly Ala
 1025 1030 1035 1040

Gly Leu Arg Gly Gly Tyr Ser Thr Val Glu Ser Leu Ser Asn Arg Asp
 1045 1050 1055

Arg Cys Arg Val Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln
 1060 1065 1070

Phe Gly Glu Cys Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys
 1075 1080 1085

Ser Tyr Gly Met Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser
 1090 1095 1100

Ser Ser Cys Asp Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro
 1105 1110 1115 1120

Asp Asp Phe Ser Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln
 1125 1130 1135

Phe Asp Pro Gly Leu Glu Tyr Lys Pro Pro Ala Val Arg Ala Pro Ala
 1140 1145 1150

Gly Gly Arg Gly Thr Asn Thr Gln Gly Ser Gly Val Gly Gly Gly Gly
 1155 1160 1165

Ser Asn Lys Asp Asp Asn Ser Leu Ser Asn Arg Asp Arg Cys Arg Val
 1170 1175 1180

Gly Gln Ile Ser Leu Tyr Asp Gly Pro Leu Ala Gln Phe Gly Glu Cys
 1185 1190 1195 1200

Gly Lys Tyr Gly Asp Leu Phe Val Ala Ala Leu Lys Ser Tyr Gly Met
 1205 1210 1215

Leu Cys Ile Gly Leu Tyr Arg Phe Arg Asp Thr Ser Ser Ser Cys Asp
 1220 1225 1230

Ala Ser Ser Lys Arg Tyr Val Ile Thr Asn Pro Pro Asp Asp Phe Ser
 1235 1240 1245

Leu Leu Pro Thr Asp Gln Val Phe Val Leu Met Gln Phe Asp
 1250 1255 1260

<210> 23
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense
 oligonucleotide

<400> 23
gtggatgata ccgacatgct ggac

24

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense
oligonucleotide

<400> 24
gagaccacct ctctcccgtg tcgt

24

<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSLo3 (S4 to
S5) sense primer

<400> 25
ctcgaactcc ctaaaatctt acagat

26

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSLo3 (S4 to
S5) antisense primer

<400> 26
ttccgttgag ccaggggtca ccagaatt

28

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mSLo3 (S8 to
S9) sense primer

<400> 27
tctgctttgt gaagctaaat ct

22

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 (S8 to S9) antisense primer

<400> 28

tttcaaagcc tcttttagcgg taa

23

<210> 29

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 (S9 to S10) sense primer

<400> 29

ttatgcctgg atctgcactc tacatg

26

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mSlo3 (S9 to S10) antisense primer

<400> 30

atagtttccg tctactaccg aaa

23

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:control human beta-actin sense primer

<400> 31

gatgatatcg ccgcgctcgt cgtcgac

27

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:control human beta-actin antisense primer

<400> 32

tccgtccagg tctgcgtcct accgtac

27

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:northern blot
sense primer

<400> 33
cggaacgctc atgtacaatc gaaatcca

28

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:northern blot
antisense primer

<400> 34
ttccggttgag ccaggggtca ccagaatt

28

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human testis
cDNA library primer

<400> 35
ggcagcgctc attctttcct cctt

24

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human testis
cDNA library primer

<400> 36
tgcccaaaac ctcaacccaa aata

24

<210> 37
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region A peptide starting at amino acid 792

<400> 37
Ile Ala Val Asn
1

<210> 38
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region A peptide ending at amino acid 870

<400> 38
Leu Thr Glu Leu
1

<210> 39
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region A peptide starting at amino acid 793

<400> 39
Arg Ala Val Asn
1

<210> 40
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region A peptide ending at amino acid 885

<400> 40
Ile Thr Glu Leu
1

<210> 41
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region B peptide starting at amino acid 871

<400> 41
Lys Asn Pro Ser
1

<400> 45
Gly Ala Ala Phe
1

<210> 46
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region C peptide starting at amino acid 899

<400> 46
Ser Thr Ser Phe
1

<210> 47
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo3 Region C peptide ending at amino acid 941

<400> 47
Ser Glu Met Glu
1

<210> 48
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region C peptide starting at amino acid 909

<400> 48
Thr Gln Pro Phe
1

<210> 49
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> PEPTIDE
<222> (1)..(4)
<223> mSlo1 Region C peptide ending at amino acid 963

<400> 49
Pro Glu Leu Glu
1

<400> 53
Glu Leu Val. Pro
1

000000"0/06T660